72. (Amended) The isolated polynucleotide of claim 71 having a coding sequence at least 98% identical to the coding sequence of SEQ ID No. 1 or its complement.

E9 cont

73. (Amended) The isolated polynucleotide of claim 72 having a coding sequence at least 99% identical to the coding sequence of SEQ ID No. 1 or its complement.

75. (Amended) An isolated polynucleotide encoding a glutathione transferase (GST) subunit having a nucleic acid sequence at least 95% identical to at least about 100 contiguous nucleotides of SEQ ID No. 1 or its complement.

E10

80. (Amended) An isolated polynucleotide encoding a glutathione transferase (GST) subunit having a sequence of SEQ ID NO:2 modified by up to about 30 conservative amino acid substitutions.

E11

REMARKS

This amendment is being filed in response to the Office Action dated October 22, 2002. Reconsideration of this application in view of the technical amendments and remarks made herein is respectfully requested.

Claims 1-4, 8-15, 20-23, 25-27, 29-32, 43, 66-80 are pending. Claims 1, 66, 67, 74 and 79 have been deleted without prejudice to pursuing the subject matter of the claims in a continuation application. Applicants have made technical amendments to claims 2-4, 8, 10, 20-23, 25-27, 29, 32, 68, 71-73, 75 and 80 and to the specification. No new matter has been added by the amendments to the claims and the specification.

In accordance with 37 C.F.R. §1.121, applicants have provided (1) accurate instructions to amend the claims, (2) replacement claims in clean form herein, and (3) another

version of the amended claims marked up to show all the changes relative to the previous version of the claims, which appears on an attached page.

I. SPECIFICATION

The Examiner has indicated that the specification lacks an Abstract. Applicants have amended the specification to include the Abstract that was published in WO 99/14337, to which this application claims priority and have directed that the abstract be added as a separate page of the specification. Accordingly, Applicants have provided the abstract on a separate page herewith.

II. CLAIM OBJECTIONS

Claims 26 and 27 are objected to because they refer to "plant cells" of claim 13 from which they depend. However, claim 13 refers to "a cell". In response, Applicants have amended claims 26 and 27 to refer to "the cell " of claim 13 and therefore, respectfully request that the objection be withdrawn.

Claims 3 and 4 are objected to as being dependent upon a rejected base claim. The Examiner has indicated that these claims would be allowable if rewritten in independent form including all the limitations of the base claim from which they depend. In response, Applicants have accordingly amended claims 3 and 4.

III. REJECTIONS UNDER 35 USC §112 ¶ 2:

Claims 20-23 and 25 are rejected under 35 U.S.C. § 112, ¶ 2 as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. The Examiner alleges that the terms "obtaining" or "obtained" are indefinite and should be replaced by the terms "producing" or "produced". Accordingly, Applicants have amended claims 20-23 and 25 to include the terms "producing" or "produced" in

place of the terms "obtaining" or "obtained". Applicants have also amended claims 27 and 32 in a similar fashion for consistency.

The Examiner alleges that claim 23 is indefinite because it refers to "a method" and should refer to "the method" of claim 21. Applicants have accordingly amended claim 23.

For all of the foregoing reasons, Applicants respectfully request that the rejections of claims 20-23 and 25 under 35 U.S.C. § 112, second paragraph, be withdrawn.

IV. REJECTIONS UNDER 35 U.S.C. § 112, FIRST PARAGRAPH

The Examiner has rejected claims 1, 2 and 8-15, 20-23, 25-27, 29-32, 43, and 66-80 under 35 U.S.C. § 112, first paragraph as containing subject matter that was not described in the specification in such a way as to enable one skilled in the art to make and use the invention. The Examiner alleges that Applicants lack a written description of the genus of polynucleotides that encode a GST subunit as broad as the genus being claimed.

Applicants respectfully disagree that the specification does not describe a genus of polynucleotides as broad as that of claims 1 and 2. Claim 1 has been limited to SEQ ID No. 1 and sequences which selectively hybridize to SEQ ID No. 1. As noted above, the specification provides a detailed description of selective hybridization. Applicants point out that the specification further teaches functional equivalents of glutathione transferase sequences related to SEQ ID No. 1. *See* pate 15, lines 20-22. In addition, the specification teaches GST sequences described in terms of strength of hybridization over background under specific hybridization conditions. *See* page 15, line 26 through page 16, line 3. The specification also teaches homologues of SEQ ID No. 1. *See* page 16, lines 8-14. Furthermore, the specification teaches GST sequences with modified nucleotides and/or backbones. *See* page 16, lines 23-27. The

specification also teaches ways to identify allelic variants of GST sequences related to SEQ ID No. 1 (page 17, lines 3-7), the properties of an allelic variant (page 21, lines 16-24), GST sequences with optimized codon usage and/or engineered restriction sites (page 18, line 29 to page 19, line 4) and how to produce conservative substitutions (page 22, lines 18-22 and the chart on page 22). Moreover, the specification also teaches 8 additional polynucleotide sequence which are species of claims 1 and 2, namely SEQ ID NOs:3, 5, 7, 9, 11, 13, 15 and 17 (as well as 8 additional polypeptide sequences, namely SEQ ID NOs:4, 6, 8, 10, 12, 14, 16 and 18). As such, Applicants assert that the specification does provide an adequate written description commensurate with the scope of claims 1 and 2. However, in order to advance prosecution of the present application, Applicants have deleted claim 1 and have amended claim 2 to depend from newly amended claims 3 and 4. Therefore, Applicants respectfully request that the rejection be withdrawn.

In addition, the Examiner has rejected claims 8-15, 20-23, 25-27, 29-32, 43, 77 and 78 under 35 U.S.C. § 112, first paragraph because the claims are allegedly directed to compositions comprising the polynucleotide of claim 1 or methods of using the same, and as such, have not been adequately described. As indicated above, Applicants assert that the polynucleotide of claim 1 is fully and adequately described in the specification. However, Applicants have cancelled claim 1 and claims 8-15, 20-23, 25-27, 29-32, 43, 77 and 78 now depend from to the polynucleotides of claim 3 or 4, which the Examiner has indicated are allowable. Therefore, Applicants respectfully request that the rejection be withdrawn.

The Examiner has also rejected claims 68-76, and 79-80 as allegedly being indefinite for reciting polynucleotides having defined percent identity to SEQ ID NO:1, of fragments thereof, allelic variations of SEQ ID NO:1 or to isolated polynucleotides encoding

modified variants of SEQ ID NO:2 at unspecified amino acids. Applicants respectfully disagree that these claims are indefinite. Applicants wish to point out that claims 74 and 79 have been cancelled. In addition, claims 68-73, 75, 76 and 80 have been amended to be directed to a polynucleotide encoding a glutathione transferase (GST) subunit. Applicants reiterate that the specification teaches functional equivalents of glutathione transferase sequences related to SEQ ID No. 1. *See* pate 15, lines 20-22. In addition, the specification teaches homologues of SEQ ID No. 1. *See* page 16, lines 8-14. The specification also teaches GST sequences with modified nucleotides and/or backbones. *See* page 16, lines 23-27. Furthermore, the specification teaches ways to identify allelic variants of GST sequences related to SEQ ID No. 1 (page 17, lines 3-7), the properties of an allelic variant (page 21, lines 16-24), GST sequences with optimized codon usage and/or engineered restriction sites (page 18, line 29 to page 19, line 4) and how to produce conservative substitutions (page 22, lines 18-22 and the chart on page 22). Moreover, the specification teaches 8 additional polynucleotide sequences which are species of claims 66-76, namely SEQ ID NOs:3, 5, 7, 9, 11, 13, 15 or 17; as well as 8 additional polypeptide sequences which are species of claims 79 and 80, namely SEQ ID NOs:4, 6, 8, 10, 12, 14, 16 or 18. Accordingly, Applicants respectfully assert that the specification does provide an adequate written description commensurate in scope of claims 68-73, 75, 76 and 79, as amended (as well as for cancelled claims 66, 67, 74 and 79) and respectfully request that the rejection be withdrawn.

The Examiner also alleges that the specification is not enabling of the full scope of claims 1, 2, 8-15, 20-23, 25-27, 29-32, 43 and 66-80. Applicants have deleted claim 1 without prejudice to pursuing the subject matter in a continuation application. In addition, Applicants have amended claims 8-15, 20-23, 25-27, 29-32 and 43 to depend from claims 3 or 4, and

therefore, Applicants assert that these claims are fully enabled. In addition, while Applicants have deleted claim 1 and amended claims 2, 8-15, 20-23, 25-27, 29-32 and 43, Applicants assert that the claims, prior to amendment, were nonetheless fully enabled for the reasons stated above with respect to the Examiner's written description rejection. In addition, and for the reasons stated above, Applicants assert that amended claims 68-73, 75-78 and 80 (as well as deleted claims 66, 67, 74 and 79) are fully enabled by the present specification.

The Examiner further alleges that the Applicants have provided limited guidance for the breadth of claims 66-76 and 80, because the claims are not directed to polynucleotides encoding a GST enzyme. Applicants point out that claims 66, 67 and 74 have been deleted without prejudice to pursuing the subject matter of the claims in continuation applications. In addition, Applicants have amended claims 68-73, 74, 76 and 80 to recite "a polynucleotide encoding a glutathione transferase (GST) subunit".

For all the foregoing reasons, Applicants respectfully request that the rejections of the claims under 35 U.S.C. § 112, first paragraph be withdrawn.

V. REJECTIONS UNDER 35 USC § 102(b)

Claims 1, 2, 8, 9, 66, 67 and 79 stand rejected under 35 USC § 102(b) as allegedly anticipated by Dudler et al., 1991, *Molecular Plant-Microbe Interactions* 4:14-18 ("Dudler"). Specifically, the Examiner alleges that Dudler discloses an isolated polynucleotide encoding a wheat GST with operably linked regulatory sequences that allow expression of the coding sequence in a plant host cell that would hybridize selectively to SEQ ID NO:1 or its complement, or is an allelic variant of the polynucleotide shown in SEQ ID NO:1.

Applicants respectfully disagree that the present claims are anticipated by Dudler. Dudler discloses the wheat gene encoding *WIR*56. Dudler further indicates that *WIR*56 shows 50% protein sequence identity to Maize GST and that it has admittedly weak GST activity. The Examiner has not provided any convincing arguments that the gene disclosed by Dudler et al. would hybridize selectively to SEQ ID NO:1 or its complement or would be considered an allelic variant of SEQ ID NO:1. In fact, given the relatively low protein sequence identity, it is likely that the polynucleotide sequence identity will be even lower. However, because Applicants have deleted claims 1, 66, 67 and 79, and have amended claims 2, 8 and 9 to be dependent from claims 3 or 4, Applicants assert that the rejection is moot and therefore, respectfully request that the rejection under 35 U.S.C. § 102(b) be withdrawn.

VI. REJECTIONS UNDER 35 USC § 102(e)

Claims 1, 2, 8-15, 20-23, 25-27, 29-32, 43, 66, 67, 74, 77 and 78 stand rejected under 35 USC § 102(e) as allegedly anticipated by McGonigle et al. (US Patent No. 5,962,229).

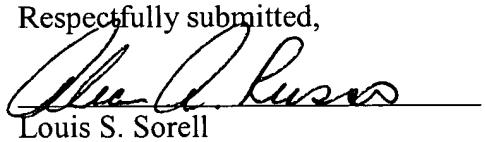
Specifically, the Examiner alleges that McGonigle discloses an isolated polynucleotide that is capable of hybridizing selectively to the coding sequence of SEQ ID No. 1, in addition to a 23 base pair fragment thereof as defined by Applicant on page 16, paragraph 2. The Examiner further alleges that McGonigle discloses a chimeric gene, vector and transformed prokaryotic and plant cells comprising said isolated polynucleotide and inherently discloses transformed plants, progeny thereof, seed thereof, and callus thereof, in addition to methods of making the same. The Examiner further alleges that McGonigle also discloses a method of controlling the growth of weeds at a locus comprising said transformed plants and therefore, McGonigle has previously disclosed all of the claim limitations of claims 1, 2 and 4.

Applicants respectfully disagree that McGonigle discloses all of the limitations of the claims of the present application and that McGonigle is also not 102(e) art because the present invention was made prior to August 11, 1997, as evidenced by the enclosed Declaration under 37 C.F.R. § 1.131 signed by co-inventor Ian Cummins. Nonetheless, Applicants have cancelled claims 1, 66, 67 and 74. In addition, Applicants have amended claims 2, 8-15, 20-23, 25-27, 29-32, 43, 77 and 78 to depend from claims 3 or 4, which the Examiner has indicated are allowable. Applicants have cancelled and amended the claims without prejudice to pursuing their subject matter in a continuation application in which Applicants acknowledge an interference may be invoked if necessary. Therefore, Applicants respectfully request that the rejection of the claims under 35 U.S.C. § 102(a) be withdrawn.

VII. CONCLUSION

In view of the amendments to the claims and the remarks herein, Applicants maintain that the Claims are now in condition for allowance. A Notice of Allowance is earnestly solicited.

Respectfully submitted,



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MARKED UP VERSION OF TECHNICAL AMENDMENTS

IN THE SPECIFICATION

Please rewrite the title as follows:

[NEW PLANT GENES] GLUTATHIONE TRANSFERASE NUCLEIC ACIDS, POLYPEPTIDES, TRANSGENIC PLANTS AND METHODS OF USE THEREOF

Please add the following abstract after page 70 of the specification:

This invention relates to glutathione transferase (GST) subunits, to nucleic acid sequences encoding glutathione transferase subunits, and to sues of these glutathione transferases and coding sequences, especially in the field of plant biotechnology.

IN THE CLAIMS

Please delete claims 1, 66, 67, 74 and 79.

Please rewrite the claims as follows:

2. (Twice Amended) The isolated polynucleotide of claim [1] 3 and 4, wherein the polynucleotide is a DNA sequence.

3. (Twice Amended) An isolated polynucleotide encoding a glutathione transferase (GST) subunit, [which polynucleotide comprises a coding sequence which hybridizes selectively to the coding sequence of SEQ ID No. 1 or to the compliment of SEQ ID No. 1. The isolated polynucleotide according to claim 1,] wherein the coding sequence encodes the amino acid sequence of SEQ ID No. 2.

4. (Twice Amended) (Twice Amended) An isolated polynucleotide encoding a glutathione transferase (GST) subunit, [which polynucleotide comprises a coding sequence which hybridizes selectively to the coding sequence of SEQ ID No. 1 or to the compliment of SEQ ID No. 1. The isolated polynucleotide according to claim 1,] wherein the polynucleotide is coding sequence of SEQ ID No. 1.

8. (Amended) A chimeric gene comprising the polynucleotide according to claim [1] 3 or 4 operably linked to regulatory sequences that allow expression of the coding sequence in a host cell.

10. (Twice Amended) A vector comprising the polynucleotide according to any one of claims [1]2 to 4 or the chimeric gene according to claim 8 or 9.

20. (Twice Amended) A method of [obtaining] producing a transgenic plant cell comprising:

(a) transforming a plant cell with the expression vector according to claim 11 to [obtain] produce a transgenic plant cell, and optionally,

(a') transforming the cell with one or more further polynucleotide sequences coding for a GST subunit, operably linked to regulatory elements that allow expression of the subunit in the cell.

21. (Twice Amended) A method of [obtaining] producing a first-generation transgenic plant comprising:

(a) transforming a plant cell with the expression vector according to claim 11 to [obtain] produce a transformed plant cell; and

(b) regenerating the transformed plant cell to [obtain] produce a transgenic plant.

22. (Twice Amended) A method of [obtaining] producing a transgenic plant seed comprising:

(a) [obtaining] producing a transgenic seed from the transgenic plant [obtained] produced by step (a) of claim 21.

23. (Amended) [A] The method of claim 21 [obtaining producing a transgenic progeny plant] comprising [obtaining] producing a second generation transgenic progeny plant from a first-generation transgenic plant [obtainable by a method according to claim 21], and optionally [obtaining] producing transgenic plants of one or more further generations from the second-generation progeny plant thus [obtained] produced.

25. (Twice Amended) A transgenic plant cell [obtained] produced by the method according to claim 20.

26. (Amended) A transgenic plant cell callus comprising [plant cells] the cell according to claim 13.

27. (Amended) A transgenic plant cell callus comprising [plant cells] the cell according to claim 13, or [obtainable] produced from a tansgenic plant cell, first-generation plant, plant seed or progeny plant according to claim 25.

29. (Amended) A nucleic acid construct comprising:

(a) the isolated polynucleotide according to claim [1] 3 or 4 operably linked to regulatory elements that allow expression of the coding sequence in a plant cell; and

(b) a site into which a further polynucleotide comprising a coding sequence can be inserted.

32. (Thrice Amended) A method of transforming a plant cell or of [obtaining] producing a plant cell culture or transgenic plant, the method comprising:

(a) providing an untransformed plant cell which is susceptible to a herbicide whose herbicidal activity is reduced by a dimeric protein comprising two GST subunits;

(b) transforming the plant cell with the vector according to claim 31;

(c) cultivating the transformed cell under conditions that allow the expression of the polynucleotide encoding a GST subunit to provide a polypeptide comprising a GST subunit, wherein the polypeptide comprising the GST subunit can form a dimer with another GST subunit; and/or

(c') regenerating the cell to give a cell culture or plant such that the polynucleotide is expressed to provide a polypeptide comprising a GST subunit, wherein the polypeptide comprising the GST subunit can form a dimer with another GST subunit;

(d) contacting the cell, cell culture or plant with the herbicide whose herbicidal activity is reduced by the dimeric protein, and to which the untransformed plant cell was susceptible, and

(e) selecting cells, cell cultures or plants that are less susceptible to the herbicide than are corresponding untransformed cells, cell cultures or plants.

69. (Amended) An isolated polynucleotide encoding a glutathione transferase (GST) subunit having a coding sequence at least 70% identical to the coding sequence of SEQ ID No. 1 or its complement.

74. (Amended) The isolated polynucleotide of claim [69] 70 having a coding sequence at least 95% identical to the coding sequence of SEQ ID No. 1 or its complement.

75. (Amended) The isolated polynucleotide of claim [69] 71 having a coding sequence at least 98% identical to the coding sequence of SEQ ID No. 1 or its complement.

76. (Amended) The isolated polynucleotide of claim [69] 72 having a coding sequence at least 99% identical to the coding sequence of SEQ ID No. 1 or its complement.

80. (Amended) An isolated polynucleotide encoding a glutathione transferase (GST) subunit [The isolated polynucleotide of claim 74] having a nucleic acid sequence at least 95% identical to at least about 100 contiguous nucleotides of SEQ ID No. 1 or its complement.

(NEW) An isolated polynucleotide encoding a glutathione transferase (GST) subunit [encoding a polypeptide] having a sequence of SEQ ID NO:2 modified by up to about 30 conservative amino acid substitutions.

ABSTRACT

This invention relates to glutathione transferase (GST) subunits, to nucleic acid sequences encoding glutathione transferase subunits, and to sues of these glutathione transferases and coding sequences, especially in the field of plant biotechnology.